



SEQUENCE LISTING

<110> PEDERSEN, ANDERS H.
ANDERSON, KIM V.
BORNAES, CLAUS

<120> FACTOR VII OR VIIA-LIKE MOLECULES #7

<130> 31-001100US

<140> 09/782,587
<141> 2001-02-12

<150> PA 2000 00218
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<150> 60/241,916
<151> 2000-10-18

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<170> PatentIn Ver. 2.1

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20 25 30

Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
260 265 270
Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
275 280 285
Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
290 295 300
Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305 310 315 320
Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
325 330 335
Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
340 345 350
Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
355 360 365
Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
370 375 380
Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385 390 395 400
Leu Arg Ala Pro Phe Pro
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<213> Homo sapiens

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<222> (115)..(1332)

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1
aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
5 10 15
aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
20 25 30
gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
35 40 45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu	309
50 55 60 65	
cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys	357
70 75 80	
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly	405
85 90 95	
tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg	453
100 105 110	
tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro	501
115 120 125	
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	549
130 135 140 145	
gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys	597
150 155 160	
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu	645
165 170 175	
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac Cys Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His	693
180 185 190	
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	741
195 200 205	
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	789
210 215 220 225	
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	837
230 235 240	
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	885
245 250 255	
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	933
260 265 270	

gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp 275 280 285	981
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu 290 295 300 305	1029
atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc Met Thr Gln Asp Cys Leu Gln Ser Arg Lys Val Gly Asp Ser Pro 310 315 320	1077
aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys 325 330 335	1125
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ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala 355 360 365	1221
acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu 370 375 380 385	1269
tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu 390 395 400	1317
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<400> 3 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu 1 5 10 15
Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys 20 25 30
Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp 35 40 45
Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln 50 55 60
Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn 65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
260 265 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
275 280 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
290 295 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305 310 315 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
325 330 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
340 345 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
370 375 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
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Leu Arg Ala Pro Phe Pro
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cassette for expression of FVII in mammalian cells

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cgagcgtac tgcagcgatc acacgggac gaaagccggac tgccgctgac acgaaggcta 480
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer
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<400> 5
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31

<210> 6
<211> 31
<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer
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<400> 6

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31

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

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<210> 8

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer
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<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer
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<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer
CBProFpr228

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<210> 11
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer
CBProFpr226

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<210> 12
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<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide tag

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1 5

<210> 13
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<212> PRT
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<220>
<223> Description of Artificial Sequence: synthetic peptide tag

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<210> 15
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic peptide tag

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<210> 16

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic peptide tag

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<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide tag

<400> 17

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 18

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide tag

<400> 18

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<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide tag

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